

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/757,67301-10-01 04CO
OIPB ~~03-0~~03-09-01
DATE: 03/14/2001
TIME: 04:18:43 #2

INPUT SET: S36507.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Wilson, James M.
Fisher, Krishna J.(ii) TITLE OF INVENTION: Method for Recombinant Adeno-Associated
Virus-Directed Gene Therapy

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Howson and Howson
(B) STREET: Spring House Corporate Cntr, PO Box 457
(C) CITY: Spring House
(D) STATE: Pennsylvania
(E) COUNTRY: USA
(F) ZIP: 19477

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/757,673
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/242,977
(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/729,061
(B) FILING DATE: 10-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kodroff, Cathy A.
(B) REGISTRATION NUMBER: 33,980
(C) REFERENCE/DOCKET NUMBER: GNVPN.019CIP2USA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 215-540-9200

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(B) TELEFAX: 215-540-5818

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10398 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65	GAATTCGCTA GCATCATCAA TAATATACCT TATTTTGGAT TGAAGCCAAT ATGATAATGA	60
66		
67	GGGGGTGGAG TTTGTGACGT GGC GCGGGG GTGGGAACGG GCGGGGTGAC GTAGTAGTGT	120
68		
69	GGCGGAAGTG TGATGTTGCA AGTGTGGCGG AACACATGTA AGCGACGGAT GTGGCAAAAG	180
70		
71	TGACGTTTTT GGTGTGCGCC GGTGTACACA GGAAGTGACA ATTTTCGCGC GGTTTTAGGC	240
72		
73	GGATGTTGTA GTAAATTTGG GCGTAACCGA GTAAGATTTG GCCATTTTCG CGGGAAAAC	300
74		
75	GAATAAGAGG AAGTGAAATC TGAATAATTT TGTGTTACTC ATAGCGCGTA ATATTTGTCT	360
76		
77	AGGGAGATCT GCTGCGCGCT CGCTCGCTCA CTGAGGCCGC CCGGGCAAAG CCCGGGCGTC	420
78		
79	GGGCGACCTT TGGTCGCCCC GCCTCAGTGA GCGAGCGAGC GCGCAGAGAG GGAGTGGCCA	480
80		
81	ACTCCATCAC TAGGGGTTCC TTGTAGTTAA TGATTAACCC GCCATGCTAC TTATCTACAA	540
82		
83	TTCGAGCTTG CATGCCTGCA GGTGCTTACA TAACTTACGG TAAATGGCCC GCCTGGCTGA	600
84		
85	CCGCCCCAAG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT AGTAACGCCA	660
86		
87	ATAGGGACTT TCCATTGACG TCAATGGGTG GAGTATTTAC GGTAAACTGC CCACTTGGCA	720
88		
89	GTACATCAAG TGTATCATAT GCCAAGTACG CCCCTATTG ACGTCAATGA CGGTAAATGG	780
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91	CCCGCCTGGC ATTATGCCCC GTACATGACC TTATGGGACT TTCCTACTTG GCAGTACATC	840
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93	TACGTATTAG TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAT CAATGGGCGT	900
94		
95	GGATAGCGGT TTGACTCACG GGGATTTCCA AGTCTCCACC CCATTGACGT CAATGGGAGT	960
96		
97	TTGTTTTGGC ACCAAAATCA ACGGGACTTT CCAAATGTC GTAACAACTC CGCCCCATTG	1020
98		
99	ACGCAAATGG GCGGTAGGCG TGTACGGTGG GAGGTCTATA TAAGCAGAGC TCGTTTAGTG	1080

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104							
105	GTAACTGGT	AAGTTTAGTC	TTTTTGTCTT	TTATTTTCAGG	TCCCGGATCC	GGTGGTGGTG	1260
106							
107	CAAATCAAAG	AACTGCTCCT	CAGTGGATGT	TGCCTTTACT	TCTAGGCCTG	TACGGAAGTG	1320
108							
109	TTACTTCTGC	TCTAAAAGCT	GCGGAATTGT	ACCCGCGGCC	GCAATTCCTG	GGGATCGAAA	1380
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111	GAGCCTGCTA	AAGCAAAAAA	GAAGTCACCA	TGTCGTTTAC	TTTGACCAAC	AAGAACGTGA	1440
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113	TTTTCGTTGC	CGGTCTGGGA	GGCATTGGTC	TGGACACCAG	CAAGGAGCTG	CTCAAGCGCG	1500
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115	ATCCCGTCGT	TTTACAACGT	CGTGACTGGG	AAAACCCTGG	CGTTACCCAA	CTTAATCGCC	1560
116							
117	TTGCAGCACA	TCCCCCTTTC	GCCAGCTGGC	GTAATAGCGA	AGAGGCCCGC	ACCGATCGCC	1620
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119	CTTCCCAACA	GTTGCGCAGC	CTGAATGGCG	AATGGCGCTT	TGCCTGGTTT	CCGGCACCAG	1680
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121	AAGCGGTGCC	GGAAAGCTGG	CTGGAGTGCG	ATCTTCCTGA	GGCCGATACT	GTCGTCGTCC	1740
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123	CCTCAAACCTG	GCAGATGCAC	GGTTACGATG	CGCCCATCTA	CACCAACGTA	ACCTATCCCA	1800
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125	TTACGGTCAA	TCCGCCGTTT	GTTCCACCGG	AGAATCCGAC	GGGTTGTTAC	TCGCTCACAT	1860
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127	TTAATGTTGA	TGAAAGCTGG	CTACAGGAAG	GCCAGACGCG	AATTATTTTT	GATGGCGTTA	1920
128							
129	ACTCGGCGTT	TCATCTGTGG	TGCAACGGGC	GCTGGGTCGG	TTACGGCCAG	GACAGTCGTT	1980
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131	TGCCGTCTGA	ATTTGACCTG	AGCGCATTTT	TACGCGCCGG	AGAAAACCGC	CTCGCGGTGA	2040
132							
133	TGGTGCTGCG	TTGGAGTGAC	GGCAGTTATC	TGGAAGATCA	GGATATGTGG	CGGATGAGCG	2100
134							
135	GCATTTTCCG	TGACGTCTCG	TTGCTGCATA	AACCGACTAC	ACAAATCAGC	GATTTCCATG	2160
136							
137	TTGCCACTCG	CTTTAATGAT	GATTTTCAGCC	GCGCTGTACT	GGAGGCTGAA	GTTTCAGATGT	2220
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139	GCGGCGAGTT	GCGTGACTAC	CTACGGGTAA	CAGTTTCTTT	ATGGCAGGGT	GAAACGCAGG	2280
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143	ATCGCGTCAC	ACTACGTCTG	AACGTCGAAA	ACCCGAAACT	GTGGAGCGCC	GAAATCCCGA	2400
144							
145	ATCTCTATCG	TGCGGTGGTT	GAAGTCACA	CCGCCGACGG	CACGCTGATT	GAAGCAGAAG	2460
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147	CCTGCGATGT	CGGTTTCCGC	GAGGTGCGGA	TTGAAAATGG	TCTGCTGCTG	CTGAACGGCA	2520
148							
149	AGCCGTTGCT	GATTCGAGGC	GTTAACCGTC	ACGAGCATCA	TCCTCTGCAT	GGTCAGGTCA	2580
150							
151	TGGATGAGCA	GACGATGGTG	CAGGATATCC	TGCTGATGAA	GCAGAACAAC	TTTAACGCCG	2640
152							

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153	TGCGCTGTTC	GCATTATCCG	AACCATCCGC	TGTGGTACAC	GCTGTGCGAC	CGCTACGGCC	2700
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157	CCGATGATCC	GCGCTGGCTA	CCGGCGATGA	GCGAACGCGT	AACGCGAATG	GTGCAGCGCG	2820
158							
159	ATCGTAATCA	CCCGAGTGTG	ATCATCTGGT	CGCTGGGGAA	TGAATCAGGC	CACGGCGCTA	2880
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161	ATCACGACGC	GCTGTATCGC	TGGATCAAAT	CTGTGATCC	TTCCCGCCCG	GTGCAGTATG	2940
162							
163	AAGGCGGCGG	AGCCGACACC	ACGGCCACCG	ATATTATTTG	CCCGATGTAC	GCGCGCGTGG	3000
164							
165	ATGAAGACCA	GCCCTTCCCG	GCTGTGCCGA	AATGGTCCAT	CAAAAAATGG	CTTTCGCTAC	3060
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167	CTGGAGAGAC	GCGCCCGCTG	ATCCTTTGCG	AATACGCCCA	CGCGATGGGT	AACAGTCTTG	3120
168							
169	GCGGTTTCGC	TAAATACTGG	CAGGCGTTTC	GTCAGTATCC	CCGTTTACAG	GGCGGCTTCG	3180
170							
171	TCTGGGACTG	GGTGGATCAG	TCGCTGATTA	AATATGATGA	AAACGGCAAC	CCGTGGTCGG	3240
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173	CTTACGGCGG	TGATTTTGGC	GATACGCCGA	ACGATCGCCA	GTTCTGTATG	AACGGTCTGG	3300
174							
175	TCTTTGCCGA	CCGCACGCCG	CATCCAGCGC	TGACGGAAGC	AAAACACCAG	CAGCAGTTTT	3360
176							
177	TCCAGTTCCG	TTTATCCGGG	CAAACCATCG	AAGTGACCAG	CGAATACCTG	TTCCGTCATA	3420
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179	GCGATAACGA	GCTCCTGCAC	TGGATGGTGG	CGCTGGATGG	TAAGCCGCTG	GCAAGCGGTG	3480
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185	CATGGTCAGA	AGCCGGGCAC	ATCAGCGCCT	GGCAGCAGTG	GCGTCTGGCG	GAAAACCTCA	3660
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187	GTGTGACGCT	CCCCGCCGCG	TCCCACGCCA	TCCCGCATCT	GACCACCAGC	GAAATGGATT	3720
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191	AGATGTGGAT	TGGCGATAAA	AAACAAC TGC	TGACGCCGCT	GCGCGATCAG	TTCA CCGTG	3840
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193	CACCGCTGGA	TAACGACATT	GGCGTAAGTG	AAGCGACCCG	CATTGACCCT	AACGCCTGGG	3900
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197	CAGATACACT	TGCTGATGCG	GTGCTGATTA	CGACCGCTCA	CGCGTGGCAG	CATCAGGGGA	4020
198							
199	AAACCTTATT	TATCAGCCGG	AAAACCTACC	GGATTGATGG	TAGTGGTCAA	ATGGCGATTA	4080
200							
201	CCGTTGATGT	TGAAGTGGCG	AGCGATACAC	CGCATCCGGC	GCGGATTGGC	CTGAACTGCC	4140
202							
203	AGCTGGCGCA	GGTAGCAGAG	CGGGTAAACT	GGCTCGGATT	AGGGCCGCAA	GAAAAC TATC	4200
204							
205	CCGACCGCCT	TACTGCCGCC	TGTTTTGACC	GCTGGGATCT	GCCATTGTCA	GACATGTATA	4260

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SEQUENCE VERIFICATION REPORT
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